

SS I mRNA

5'——AAA 3' 5'——AAA 3' 5'——AAA 3'

SS II' mRNA

3' 5' — [] — AAA 3'

SS 5' mRNA

5' ————— AAA 3'

Preprosomatostatin

Preprosomatostatin II'

Preprosomatostatin II'

-24 . 35

H₃N- -24 | -23 | -22 | -21 -20 -19 -18 -17 -16 -15 -14 -13 -12 -11 -10 -9 -8 -7 -6 -5 -4 -3 -2 -1 35 -CCO

SS-25

SS-1.

SS-29-II

SS-1

SS-25-II

SS-1-

故此，我們在這裏所說的「人」，就是指「人」這一個體，而並非指「人」這一個別的東西。

Title: SOMATOSTATINS AND METHODS

Applicant(s): Mark Sheridan et al.

Serial No.: Unassigned Docket No.: 255.0004 0101

Filed: Herewith

Sheet 2 of 8

PPSS - I

SEQ 10 No: 8 5' GGGGGGGGGGGGACAGGAGCAGCAGAACTCAAGAGAAGCCAATCTAACGATTGTCTGCCCAATTGAACCACCTTATCC 61

ATCCTCTGCCCTCCCCCAGAGCCCAGAAGAG ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC 152
 SEQ 10 No: 3 Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu -86

TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG TCC GAT GCC AAA CTC CGC CAG CTG 214
 Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu -67

CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG 272
 Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu -46

CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC 340
 Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly -25

GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT 403
 Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu Arg Ala Pro Gly Pro Val Leu Ala Pro Arg -4

↓
 GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC 466
 Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys ***

CTTTACTGTGTACTACATCTCATCTCTTTGTTCAATCACTCATGGCTGAATCCAATGCACCATGGCTTAACCCCTCTCT 549
 TCAAAAAAATTTAAATAAACACTGTTAACATTAAACATCAATTCTGATGTTCTATCGCTCACTTAGATTTTCCGAAAAG 632
 GAACACAAGAAAGAATGTTACAAATGATGCGGTTCTGCTTGTACTGTGATTTATGTATTTGGCAGACTATTTAATTG 715
 TTTGTTGAAATGAAATCTGTGTTCAAGAACCAAAAAAA 3'

Fig. 2

PPSS-II' and PPSS-II"

SEQ ID NO:14 PPSS-II'
SEQ ID NO: 20 PPSS-II"

accaggcctgtccataccgactgtccagatcgagcatagccggccagctcagctgtctccaccegggtggcc 75
accaggcctgtccatccatcaactgatcgatccacccggccagcttagc*****acgtgtctgg 70

PPSS-II'
PPSS-II"

ccctgcaaaacaaaacccatgtctgtggag ATG AAG GTC TGC CGA ATC CAC TGT GCC CTG GCC 139/-91
ccctgcaaaacccaaactcagtcgtctgtggag ATG AGG GTC TCC CAA ATC CAC TGT GCA CTG GCC 134/-87

SEQ ID NO:15 Met Arg Val Ser Gln Ile His Cys Ala Leu Ala

PPSS-II'
PPSS-II"

CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC GCC TCG CAG CCC GAC CTG 196/-72
CTG CTG GGT CTG GCC CTG GCA ATT TGC AGC CAA GGA GCC GCC TCG CAG CCA GAC CTG 191/-68
Leu Leu Gly Leu Ala Leu Ile Cys Ser Gln Gly Ala Ala Ser Gln Pro Asp Leu

PPSS-II'
PPSS-II"

GAC CTC CGC AGC CGC AQA CTC CTT CAG AGG GCT CGT GCA TTG CCA CAC AGG 253/-53
GAC CTC CGC AGC CGC CGA CTC CTC CAG AGG GCC CTG GCC GCT GCA TTG CCA CAC AGG 248/-49
Asp Leu Ala Ser Arg Arg Leu Leu Gln Arg Ala Leu Ala Ala Leu Pro His Arg

PPSS-II'
PPSS-II"

AGT GGA GTA AGC GAG CGG TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG *** *** 304/-35
AGT GGA GTA AGC GAG CGA TGG AGG ACA TTC TAT CCG AAC TGT CCT TGC CTG AGG TGG 305/-30
Ser Gly Val Ser Glu Arg Trp Arg Thr Phe Tyr Pro Asn Cys Pro Cys Leu Arg Trp

PPSS-II'
PPSS-II"

AGG CCC AGG AAA GTG AAG TGT CAA *** GCG GGG GCT AAA GAG GAC CTG CGT GTG GAG 358/-18
AGG CCC AGA AAA GTG AAG GGT CCA CAG CTG AAG GCC AAA GAG GAC *** *** *** *** 350/-14
Arg Pro Arg Lys Val Lys Gly Pro Gln Leu Lys Ala Lys Glu Asp

PPSS-II'
PPSS-II"

Gly Asn Pro Asn
CTG GAG CGC TCA GTG GGC AAC CCC AAC AAC CTT CCC CCC CGT GAG CGC AAA GCC GGC 415/+2
CTG GAG CGC TCA GTG GAC *** *** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC 398/+2
Leu Glu Arg Ser Val Asp Asn Leu Pro Pro Arg Glu Arg Lys Ala Gly

PPSS-II'
PPSS-II"

TGC AAG AAC TTC TAC TGG AAG GGC TTC ACT TCC TGC tga gggaaagaataaaccgaccaccc 477
TGC AAG AAC TTC TAC TGG AAG GGA TTC ACT TCT TCC taa gggaaagaaaagctgaccaccc 460
Cys Lys Asn Phe Tyr Trp Lys Gly Phe Thr Ser Cys ###

PPSS-II'
PPSS-II"

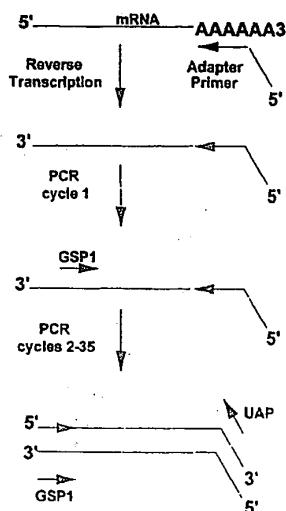
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atgacacaatgcattcaatcacatcacccgccaaccttcatctgactaatgtagccaaatcagcaatttagctgtg 535

PPSS-II'
PPSS-II"

cccgatgtatggttttggaaatcaacagaatgtatgtacccgtctaaatgtgaaataaaatataaaaaatgt(a)n
cctgatgacaattatgattatgtatgtacccgtactaaatgtgaaataaaatggagaaatggagaaac(a)n

Fig. 3

Phase I



Phase II

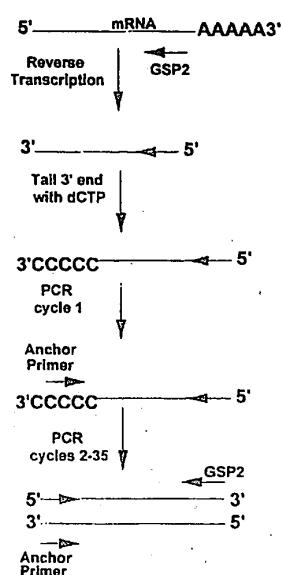


Fig. 4

000-222-222-4284-000

Nucleotide Identity

TRI	82.8	49.0	43.7	52.3	51.0	52.0	51.5	51.1	52.8	54.5
84.1	TRI	48.2	39.1	44.9	50.0	50.0	49.5	48.0	49.8	52.5
45.5	43.9	TRI	58.1	77.0	67.7	68.9	67.9	69.4	69.4	72.5
35.6	35.6	52.3	AP	60.1	58.8	55.1	53.8	55.3	56.8	56.8
44.7	40.9	73.5	52.3	CE	65.7	68.7	67.7	68.4	67.7	72.2
47.7	44.7	70.5	49.2	64.4	TRI	75.0	74.5	62.6	75.5	78.3
42.4	38.6	66.7	46.2	63.6	78.8	C	84.1	84.3	84.3	
42.4	38.6	65.2	45.5	62.9	78.0	87.9	R	92.4	91.2	92.2
42.4	38.6	66.7	46.2	63.6	78.8	88.6	97.0	B	94.4	95.5
42.4	38.6	64.4	46.2	62.9	78.8	90.9	96.2	98.5	M	98.7
45.5	42.4	73.5	47.7	68.2	87.1	91.7	97.7	98.5	100	H

Amino Acid Identity

Fig. 5

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin 1^a

	-20	-10	+10	+14
Rainbow trout ^b		A P G * * P V L A P R E R K A G C K N F P W K T F P T S C S E Q I D N O ; 4		
Hagfish ^d	A V E R P R Q D G Q V H E P P G R E R K A G C K N F P W K T F P T S C S E Q I D N O ; 27			
Lamprey ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Torpedo ^d	A G C K S P F P W K T F P T S C S E Q I D N O ; 38			
Ratfish ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 29			
Bowfin ^d	A P C K N F P W K T F P T S C S E Q I D N O ; 30			
Surgeon ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Catfish ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Salmon ^d	A A S G G P L L A P R E R K A G C K N F P W K T F P T S C S E Q I D N O ; 31			
Anglerfish ^c	A G C K N F P Y W K G F T S C S E Q I D N O ; 2			
Eel ^d	A G C K N F Y W K G F T S C S E Q I D N O ; 2			
Flounder ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Sculpin ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Frog ^c	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Salamander ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Alligator ^d	A G C K N F P W K T F P T S C S E Q I D N O ; 1			
Pigeon ^d	S A N S N P A M A P R E R K A G C K N F P W K T F P T S C S E Q I D N O ; 32			
Ovine ^d				

SEQUENCE COMPARISON

SEQ ID NO: 9	TRII'	---MKVCRTHCALAIIGLALATCSQGAASQP-----	DLDLRSRRIIQLORARAIAAWPHRSGVSE
SEQ ID NO: 15	TRII"	---MRVSQTHCALAIIGLALATCSQGAASQP-----	DIDIASRRIIQLORALAALPHRSGVSE
SEQ ID NO: 36	CFII	---MSSSPLRLALALMCIJSAGVVISCGRP-----	HVVLNSAIEEARNVPGFEEVPERLT
SEQ ID NO: 37	AFII	---MOCTRPAAIHALAATVLCGSPVSQLDREQSDNQDLDIEIROHWWITERARSAGLSQEWSKRA	
SEQ ID NO: 38	GFII	---MRLCELHCYKATIGLSEVLCGRCAANSQL--EP-----	DIDFRHIIRLIQRASATGQATQDFTKRD
SEQ ID NO: 39	GFIII	---MQLLSSHVSLLVLVLYSVRAAVAL-----	PVEERNPAQSRELSKE-RKELILKL
SEQ ID NO: 40	FRII	---MLGSAGTILLILLAW-GAPALSQ-----	PDNDNRTTGRNQDLNAIQQDLLLKL
SEQ ID NO: 3	TRI	---MLSTRVQCALAIISSLAATSSVSAAPS-----	DAKLRLQIQLORSIMAPAGKQELARNT
SEQ ID NO: 41	CFI	---MPSTKIQCALAIIAVPLSVCSVSGAPS-----	DAKLRLQIQLORSILAPSVKQELTRYT
SEQ ID NO: 42	AFI	MKMKVSSSRLRCLLVLITLSTASISCSFAGQR-----	DSKLRLLIIHRYPLQGS-KQDMTRSA
SEQ ID NO: 43	GFI	---MLSTRIQCALAIISSLAACVCSVSAAPT-----	DAKLRLQIQLORSLLNPAGKQELARYT
SEQ ID NO: 44	FRI	---MQSCRVQCALAIISSLAATNSISAAPT-----	DPRRLRQFIQKSLAAGKQELAKYF
SEQ ID NO: 45	C	---MLSCRLOCALAIIALCIVLALGGVTGAPS-----	DPRRLRQFIQKSLAAGKQELAKYF
SEQ ID NO: 46	R	---MLSCRLOCALAIIAISIVLALGGVTGAPS-----	DPRRLRQFIQKSLAAGKQELAKYF
SEQ ID NO: 47	B	---MLSCRLOCALAIIAISIVLALGCVTGAPS-----	DPRRLRQFIQKSLAAGKQELAKYF
SEQ ID NO: 48	M	---MLSCRLOCALAIIAISIVLALGCVTGAPS-----	DPRRLRQFIQKSLAAGKQELAKYF
SEQ ID NO: 49	H	---MLSCRLOCALAIIAISIVLALGCVTGAPS-----	DPRRLRQFIQKSLAAGKQELAKYF

(continued)

WRTEYPNCPLR--PRKVKCP-AGAKE-DLR--VEIERSVGN-PNNLPPRERKAGCKNEWIKGETSC
 WRTEYPNCPLRVRPRKVKGPDIAKAKE-DL-----EHSV-----DNLPPRERKAGCKNEWIKGETSC
 LPELQW-MLSNNELTPVQVEEAPRS-----RLEIYRRDN-----T-VTSKPLNCMNYFWKSRLAQC
 VEELLAQMSLPEATFQREAEADASHATE-G--RNNIERSVDS-TNNIUPPRERKAGCKNEWIKGETSC
 VEKLLSLLSIPEHEMR--EKGLSMAGE-SEDLRLEOERSAES-SNQLPTRLRKEGCKNEWIKGETSC
 ISGLLD--GVDNVSVDGEIAPVPFDAEPELESRL-EFAYVNRLSQLEQRDRKAPKNEFWKTEITSC
 LSGWTD--S-RESNLVEVERNYPOPPE-P-----KIPPSVK--FPRISLRERKAPCKNEFWKTEITSC
 LVELLS-ELAHYNEAEIELDDMSHGVE-QEDVULELERAPG--PVLAPRERKAGCKNEFWKTEITSC
 LAELLA-ELAEEAENEVLDSEVSRRAAE-SEGARLEMBRAAG--PMIAPRERKAGCKNEFWKTEITSC
 LAELLS-ELAELLS-ELVQAEANEALEEEENPLAEGGPEDAHADLERAAAG-GPLIAPRERKAGCKNEFWKTEITSC
 LAELLS-ELVQAEANEALEPEDLSRÄVE-KDEVRLELERAAAG--PMIAPRERKAGCKNEFWKTEITSC
 LAELLS-EPSSQTDNEALESDOLPRGAE-QDEVRLELERAANS-SPALIAPRERKAGCKNEFWKTEITSC
 LAELLS-EPSSOTENEAELESEDLSRGAE-QDEVRLELERAANS-NPAAIAPRERKAGCKNEFWKTEITSC
 LAELLS-EPHQQTENDALEPEDLPQAAE-QDEMRLELORSANS-NPAMAPRERKAGCKNEFWKTEITSC
 LAELLS-EPNQTEIIDALEPEDLSQAAE-QDEMRLELORSANS-NPAMAPRERKAGCKNEFWKTEITSC
 LAELLS-EPNQTEIIDALEPEDLSQAAE-QDEMRLELORSANS-NPAMAPRERKAGCKNEFWKTEITSC
 LAELLS-EPHQQTENDALEPEDLSQAAE-QDEMRLELORSANS-NPAMAPRERKAGCKNEFWKTEITSC

Fig. 7

20140228-202520262600

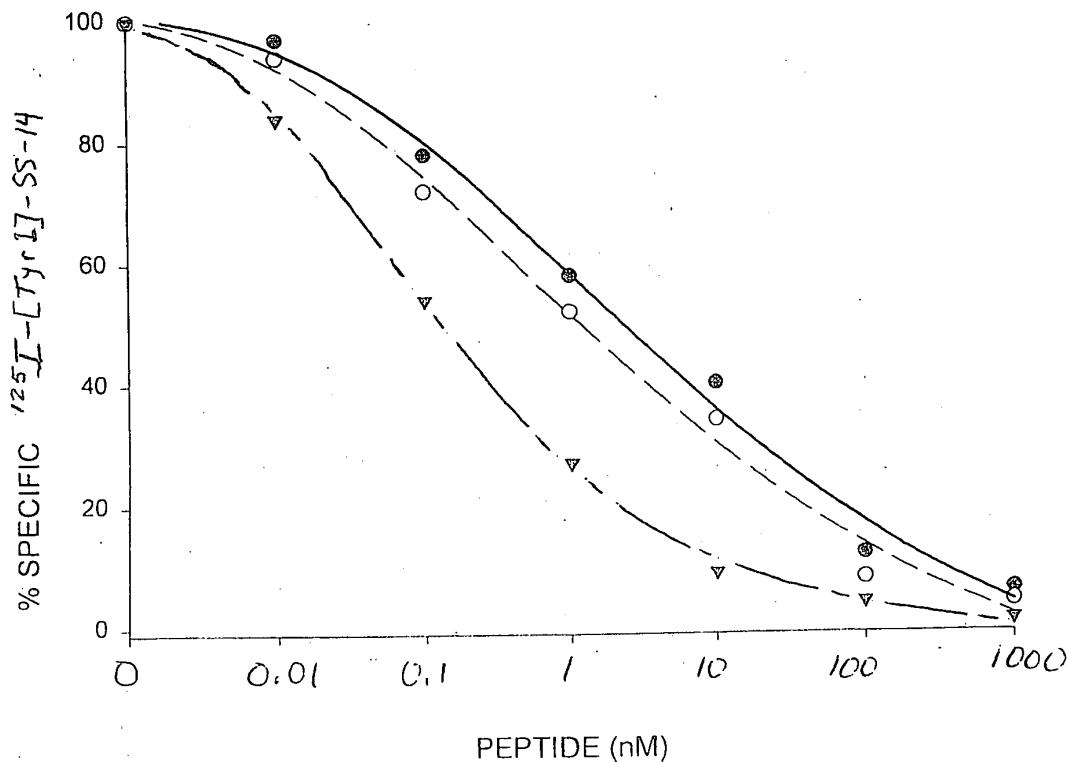


Fig. 8